#2 OIPE

RAW SEQUENCE LISTING DATE: 10/16/2001 PATENT APPLICATION: US/09/964,667 TIME: 15:24:03

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964667.raw

SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
      6
             (i) APPLICANT: de la Monte, Suzanne
      7
                             Wands, Jack R.
            (ii) TITLE OF INVENTION: Transgenic Animals and Cell The for Screening Drugs Effective for the Treatment or Prevention
      9
     10
                                       of Alzheimer's Disease
     11
     13
           (iii) NUMBER OF SEQUENCES: 14
     15
            (iv) CORRESPONDENCE ADDRESS:
     16
                   (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
     17
                   (B) STREET: 1100 New York Ave., Suite 600
     18
                   (C) CITY: Washington
     19
                   (D) STATE: DC
                   (E) COUNTRY: USA
     20
                   (F) ZIP: 20005-3934
     21
     23
             (.V) COMPUTER READABLE FORM:
                   (A) MEDIUM TYPE: Floppy disk
     24
     25
                   (B) COMPUTER: IBM PC compatible
                   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     26
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     27
     29
            (vi) CURRENT APPLICATION DATA:
                   (A) APPLICATION NUMBER: US/09/964,667 ₱₩
C--> 30
                   (B) FILING DATE: 28-Sep-2001
C--> 31
     32
                   (C) CLASSIFICATION:
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     35
                   (A) NAME: Esmond, Robert W.
                   (B) REGISTRATION NUMBER: 32,893
     36
     37
                   (C) REFERENCE/DOCKET NUMBER: 0609.4370000
            (ix) TELECOMMUNICATION INFORMATION:
     39
                   (A) TELEPHONE: 202-371-2600
     40
     41
                   (B) TELEFAX: 202-371-2540
        (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     46
                   (A) LENGTH: 1442 base pairs
     47
     48
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
     49
     50
                   (D) TOPOLOGY: both
     52
            (ii) MOLECULE TYPE: cDNA
     55
            (ix) FEATURE:
     56
                   (A) NAME/KEY: CDS
     57
                   (B) LOCATION: 15..1139
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                    50
     62 TTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
     63
                         Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
     64
                                            5
     66 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC
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     67 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
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PATENT APPLICATION: US/09/964,667

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- 68			15					20					25				
	GAT	TCT		GCC	TCA	GCC	TCC	CCA	GTA	GCT	GGG	ATT	ACA	GGC	ATG	TGC ·	146
71	Asp	Ser	Pro	Ala	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	
72		30					35					40					•
															GAG		194
		His	Ala	Arg	Leu		Leu	Tyr	Phe	Phe		Val	Glu	Met	Glu		
76	45			~~~		50					55			a	a	60	0.40
															GAT		242
80	ьeu	HIS	vaı	GIY	65	Ата	GIY	Leu	GIU	леu 70	Pro	Thr	ser	Asp	Asp 75	Pro	
	ጥሮር	стс	ሞሮਫ	GCC		$C\Delta\Delta$	ΔСΨ	േന	ΔGΔ		AGG	ΔСΨ	GGC.	CAC	CAT	GCC	290
															His		250
84				80					85	-1-	5		1	90			
86	CGG	CTC	TGC	CTG	GCT	AAT	TTT	TGT	GGT	AGA	AAC	AGG	GTT	TCA	CTG	ATG	338
87	Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	
88			95					100					105				
90	TGC	CCA	AGC	TGG	TCT	CCT	GAG	CTC	AAG	CAG	TCC	ACC	TGC	CTC	AGC	CTC	386
	Cys		Ser	\mathtt{Trp}	Ser			Leu	Lys	Gln	Ser		Cys	Leu	Ser	Leu	
92		110					115					120					
															TTT		434
		гуѕ	Cys	Trp	Asp	_	Arg	Arg	Ата	Ата		Pro	GIĀ	Leu	Phe		
	125	mmm	mmm	mma	7.77	130	N.C.C	mcm	ccc	A CITI	135	N C C	CAC	CAM	GAA	140	482
															Glu		402
100		FIIC	FILE	шец	145		лгу	СуЗ	rio	150		1111	GIII	нэр	155		
		TGG	TGT	' САТ			ጥሮል	CITIC	03.0			3.00					
							T CU		CAG	CCI	TCA	ACI	' CC1	. GAC	3 ATC	AAG	530
	3 Glr															AAG Lys	530
104					His					Pro					ı Ile		530
104	4	Trp	Cys	160	His	Ser	Ser	Leu	Gln 165	Pro	Ser	Thr	Pro	Glu 170	ı Ile	Lys	530
104 106	4 6 CAT	Trp	Cys CCI Pro	Asp 160 GCC Ala	His TCA	Ser GCC	Ser TCC	Leu	Gln 165 GTA	Pro GCI	Ser	Thr	Pro AAA	Glu 170 GAG S Asp	ı Ile	Lys CAC	
104 106 107	4 6 CAT 7 His 8	Trp	Cys CCI Pro 175	Asp 160 GCC Ala	His TCA Ser	Ser GCC Ala	Ser TCC Ser	CAA Gln 180	Gln 165 GTA Val	Pro GCT Ala	Ser GGG Gly	Thr ACC Thr	Pro AAA Lys 185	Glu 170 A GAG S Asp	I Ile	Lys CAC His	578
104 106 107 108	4 5 CAT 7 His 8 0 CAC	Trp	Cys CCI Pro 175	Asp 160 GCC Ala TGG	His TCA Ser	Ser GCC Ala	Ser TCC Ser	CAA Gln 180 ATT	Gln 165 GTA Val	Pro GCT Ala	Ser GGG Gly	Thr ACC Thr	Pro AAA Lys 185	Glu 170 A GAO S Asp	I Ile O C ATG O Met	Lys CAC His	
104 106 107 108 116	4 6 CAT 7 His 8 0 CAC 1 His	Trp CCT Pro TAC	Cys CCI Pro 175 ACC	Asp 160 GCC Ala TGG	His TCA Ser	Ser GCC Ala	TCC Ser TTT Phe	CAA Gln 180 ATT	Gln 165 GTA Val	Pro GCT Ala	Ser GGG Gly	ACC Thr AAT AAT	AAA Lys 185	Glu 170 A GAO S Asp	I Ile	Lys CAC His	578
104 106 108 116 113	4 5 CAT 7 His 8 0 CAC 1 His	Trp CCT Fro TAC Tyr 190	CYS CCI Pro 175 ACC Thr	Asp 160 GCC Ala TGG	His TCA Ser CTA	GCC Ala ATT	TCC Ser TTT Phe 195	CAA Gln 180 ATT	Gln 165 GTA Val	GCT Ala ATT	GGG Gly TTT Phe	ACC Thr AAT ASD 200	AAAA Lys	Glu 170 GAC GAC GAC TTC TTC	I Ile D ATG D Met G AGA	CAC His CAG Gln	578 626
104 106 107 108 110 111 112	4 6 CAT 7 His 8 0 CAC 1 His 2 4 AGT	Trp CCT Fro TAC Tyr 190	CYS CCT Pro 175 ACC Thr	Asp 160 GCC Ala TGG Trp	His TCA Ser CTA Leu	Ser GCC Ala ATT Ile	TCC Ser TTT Phe 195 CAG	CAA Gln 180 ATT Ile	Gln 165 GTA Val TTT Phe	GCT Ala	Ser GGG Gly TTT Phe	ACC Thr AAT ASN 200	Pro AAA Lys 185 TTT	Glu 170 GAC GAC GAC TTC E Leu	I Ile C ATG Met G AGA Arg	CAC His CAG Gln	578
104 106 107 108 116 117 114 114	4 6 CAT 7 His 8 0 CAC 1 His 2 2 4 AGT	Trp CCT TAC Tyr 190 CTC	CYS CCT Pro 175 ACC Thr	Asp 160 GCC Ala TGG Trp	His TCA Ser CTA Leu	Ser GCC Ala ATT Ile ACC	TCC Ser TTT Phe 195 CAG Gln	CAA Gln 180 ATT Ile	Gln 165 GTA Val TTT Phe	GCT Ala	Ser GGG Gly TTT Phe CAG	ACC Thr AAT ASn 200 TGG	Pro AAA Lys 185 TTT	Glu 170 GAC GAC GAC TTC E Leu	I Ile C ATG Met G AGA Arg	CAC His CAG Gln	578 626
104 106 107 116 117 117 118	4 5 CAT 7 His 8 0 CAC 1 His 2 2 4 AGT 5 Ser 7 205	Tre CCTAC TAC Tyr 190	CYS CCI Pro 175 ACC Thr AACC AACC AACC	Asp 160 GCC Ala TGG Trp	C TCA C TCA C Ser C CTA C Leu C GTC	Ser GCC Ala ATT Ile ACC Thr 210	TCC Ser TTT Phe 195 CAG	CAA Gln 180 ATT Ile GCT Ala	Gln 165 GTA Val TTT Phe GGA	Pro GCT Ala ATT Ile GTG	Ser GGG Gly TTT Phe CAG Gln 215	Thr ACC Thr AAT Asn 200 TGG	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Glu 170 A GAO B Asp TTO E Leu C AAT	I Ile	CAC His CAG Gln GGC Gly 220	578 626
104 106 107 108 116 117 117 117	4 5 CAT 7 His 8 0 CAC 1 His 2 4 AGT 5 Ser 7 205 9 TC	Tree CCT TAC TYPE CTC CTC CTC CTC CTC CTC CTC CTC CTC CT	CAACO	Asp 160 GCC Ala TGG Trp TCT Ser	His CTCA Ser CTA Leu CTC Val	Ser GCC Ala ATT Ile ACC Thr 210	TCC Ser TTT Phe 195 CAG Gln	CAA Gln 180 ATT Ile GCT Ala	Gln 165 GTA Val TTT Phe GGA Gly	Pro GCT Ala ATT Ile GTG Val	Ser GGG Gly TTT Phe CAG Gln 215	Thr ACC Thr AAT Asn 200 TGG Trp	Pro AAA 185 17TT Phe CGG Arg	Glu 170 GAG S ASE TTC Let LAT ASE TTC TTC TTC TTC TTC TTC TTC TTC TTC TT	I Ile	CAC His CAG Gln GGC Gly 220 AGC	578 626 674
104 106 107 108 116 117 117 117	4 5 CAT 7 His 8 0 CAC 1 His 2 4 AGT 5 Ser 7 205 9 TCA 0 Ser	Tree CCT TAC TYPE CTC CTC CTC CTC CTC CTC CTC CTC CTC CT	CAACO	Asp 160 GCC Ala TGG Trp TCT Ser	His CTCA Ser CTA Leu CTC Val	Ser GCC Ala ATT Ile ACC Thr 210 CCT Pro	TCC Ser TTT Phe 195 CAG Gln	CAA Gln 180 ATT Ile GCT Ala	Gln 165 GTA Val TTT Phe GGA Gly	Pro GCT Ala ATT Ile GTG Val	GGG GGG Gly TTT Phe GCAG Gln 215 TTA	Thr ACC Thr AAT Asn 200 TGG Trp	Pro AAA 185 17TT Phe CGG Arg	Glu 170 GAG S ASE TTC Let LAT ASE TTC TTC TTC TTC TTC TTC TTC TTC TTC TT	I Ile C ATG D Met G AGA I Arg C CTI I Leu	CAC His CAG Gln GGC Gly 220 AGC Ser	578 626 674
104 106 107 116 117 117 118 120 121	4 6 CAT 7 His 8 0 CAC 1 His 2 2 4 AGT 5 Ser 7 205 9 TCA 0 Ser 1	Try TAC TAC TYP 190 CTC Leu CTC Leu CTC	C CYS CCT Pro 175 C ACC Thr ASD ASD C AAC	Asp 160 GCC Ala TGG Trp TCT Ser	His TCA Ser CTA CTA CTA Val	GCC Ala ATT Ile ACC Thr 210 CCT Pro	TCC Ser TTT Phe 195 CAG Gln CCC	CAA Gln 180 ATT Ile GCT Ala	Gln 165 GTA Val TTT Phe GGA Gly	GCT Ala Ile Ile Val	GGG Gly TTT Phe CAG Gln 215	Thr ACC Thr AAT ASN 200 TGG Trp	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GRUENT TO THE LEVEL AND AST	I Ile O ATG O Met G AGA I Arg C CTT I Leu C CCC S Pro 235	CAC His CAG Gln GGC Gly 220 AGC Ser	578 626 674
104 106 107 116 117 117 117 119 120 121 121	4	Trp CCTAC TAC TYP 190 CCTC Leu CCTC	CYS CYS CYS CYS TO	Asp 160 GCC Ala TGG Trp TCT Ser CCT	His TCA Ser CTA CTA CTA Val	GCC Ala ATT Ile ACC Thr 210 CCT Pro	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAAGIN 180 ATTILE GCT Ala	Gln 165 GTA Val TTT Phe GGA Gly TTC	GCT Ala GTG Val	GGG Gly TTT Phe CAG Gln 215 TTA Leu	Thr ACC Thr AAT ASN 200 TGG Trp	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GREAT TO AST AST CONTRACT CONT	I Ile O ATG O Met G AGA I Arg C CTT I Leu C CCC S Pro 235	CAC His CAG Gln GGC Gly 220 AGC Ser	. 578 626 674 722
104 106 107 116 117 117 118 126 127 128 128	4	Trp CCTAC TAC TYP 190 CCTC Leu CCTC Leu CCTC	CYS CCT Pro 175 CACC Thr ASD CAAC GAAC GAAC GAAC GAAC GAAC GAAC GAA	Asp 160 GCC Ala Trp TCT Ser CCT AGC	His TCA Ser CTA CTA CTG Val	GCC Ala ATT Ile ACC Thr 210 CCT Pro	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAGIN 180 ATT Ile GCT Ala GGG Gly AGG Arg	Gln 165 GTA Val TTT Phe GGA Gly TTC Phe CGC	GCT Ala GTG Val	GGG Gly TTT Phe CAG Gln 215 TTA Leu	Thr ACC Thr AAT ASN 200 TGG Trp The	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GREAT TO THE LET TO TH	I Ile ATG Met AGA ATG CTT Leu CCCC 235 AATG ASD	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe	578 626 674 722 770
104 100 100 110 111 112 113 114 115 126 127 128 129 129 129	4	Try CTAC TAC TYY 190 CTC Leu CTC Leu CTC Leu CTC CTC	CYS CCT Pro 175 ACC Thr ASD CAAC ASD CAAC GAAC GAAC GAAC GAAC GAAC GAAC GAA	Asp 160 GCC Ala Trp TCT Ser CCT Pro	His TCA Ser CTA CTA CTA CTA CTA CTG CTA CTG CTA	GCC Ala ATT Ile ACC Thr 210 CCT GAC Asp	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAAGIN 180 ATT Ile GCT Ala GGG Gly AGG	Glm 165 GTA Val TTTT Phe GGA Gly TTC CGC Arg 245	GCT Ala GTG Val	Ser GGG Gly TTTT Phe CAG Gln 215 TTA Leu CCA Pro	Thr ACC Thr AAT ASN 200 TGG Trp Phe	AAP Lys 185 TTT Phe CGC Arg	GIU 170 GAC GAC GAC TTC E Leu C AAT ASI C TGC C YS A GCT A Ala 250 C AGC	I Ile ATG Met AGA ATG ATG Met CTT Leu CCC Prc 235 AATG ASn TTG	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe	. 578 626 674 722
104 106 107 116 117 117 117 118 120 121 122 122 123 124 125	4 CAT His B CAC His CA	Try CTAC TAC TYY 190 CTC Leu CTC Leu CTC Leu CTC CTC	CYS CCT Pro 175 ACC Thr ASD CAAC ASD CAAC GAAC GAAC GAAC GAAC TTT FRE	Asp 160 GCC Ala Trp TCT Ser CCT Pro Ser 240 TTA	His TCA Ser CTA CTA CTA CTA CTA CTG CTA CTG CTA	GCC Ala ATT Ile ACC Thr 210 CCT GAC Asp	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAAGIN 180 ATT Ile GCT Ala GGG Gly AGG Gly GGG Gly	Glm 165 GTA Val TTTT Phe GGA Gly TTC Phe CGC Arg 245 TTC Phe	GCT Ala GTG Val	Ser GGG Gly TTTT Phe CAG Gln 215 TTA Leu CCA Pro	Thr ACC Thr AAT ASN 200 TGG Trp Phe	AAP Lys 185 TTT Phe CGC Arg	GIU 170 GAC GAC GAT TTC E Leu C AAT ASI C TGC C YS A GCT A A La 250 C AGC A A SI	I Ile ATG Met AGA ATG CTT Leu CCCC 235 AATG ASD	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe	578 626 674 722 770
104 100 100 110 111 112 113 114 115 126 127 128 129 129 129 129	4 CAT His B CAC His CA	Try TAC TAC TYP 190 CTC Leu CTC Leu CTC TC	CYS CCT Pro 175 ACC Thr AS AS AS AS AS AST ATT Phe 255	Asp 160 GCC Ala TGG Trp CTCT Ser AGC Ser 240 TTA Leu	CTA	Ser GCC Ala ATT Ile ACC Thr 210 CCT Pro GAC Asp	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAAGIN 180 ATT Ile GCT Ala GGG Gly AGG Gly 260	Glm 165 GTA Val TTT Phe GGA Gly TTC Phe CGC Arg 245 TTC	GCT Ala GTG Val	GGG Gly TTT Phe CAG Gln 215 TTA Leu CCA Pro	Thr ACC Thr AAT ASN 200 TGG Trp CGC Arg	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GIU 170 GAC GAC GAC TTC E Leu C AAT ASI C TGC C Cys A GCT A A La 250 A A C A A A C A A A A	I Ile ATG Met AGA AGA ATG CTT Leu CCCG Pro 235 AAT AASn TTG Leu	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe ATC	578 626 674 722 770 818
104 100 107 110 111 112 113 114 115 120 122 122 123 123 124 133	4 CAT His B CAC His CA	Try CTAC TAC TYP 190 CTCC Leu CCTCC Leu CCTCC CTAC CTCC CTCC CTCC CTCC CTCC CT	CYS CYS CYS CYS TOTAL ACC ACC ACC ACC ACC ACC ACC ACC ACC A	Asp 160 GCC Ala Trp TCT Ser CCT Pro 240 TTA Leu	His TCA Ser CTA CTA CTA CTG TCTG TTCG TTCG TCTG CTA CTA	Ser GCC Ala ATT Ile ACC Thr 210 CCT Pro GAC GAC GAC GLU	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAAGIN 180 ATT Ile GCT Ala GGG Gly 260 CTG	Gln 165 GTA Val TTT Phe GGA Gly TTC Phe 245 TTC Phe	GCT Ala GTG Val	Ser GGG Gly TTT Phe CAG Gln 215 TTA Leu A CCA Pro	Thr ACC Thr AAT ASN 200 TGG Trp CGC Phe	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GIU 170 GAC GAC GAT C TTC C AAT A ASI C TGC C Cys A GCT A AC 250 A AC 250 A 250 A AC 250 A AC 250 A 250 A AC 250 A 25	I Ile ATG Met AGA AGA CTT Leu CCC AATG CTT AATG A	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe ATC Ile	578 626 674 722 770
104 100 107 110 111 112 113 114 115 120 122 122 123 123 124 133	4	Try CTAC TAC TYP 190 CTCC Leu CCTCC Leu CCTCC CTAC CTCC CTCC CTCC CTCC CTCC CT	CYS CCT Pro 175 ACC Thr ASn CAAC GAAG GAAG GAAG GAAG GAAG GAAG GAA	Asp 160 GCC Ala Trp TCT Ser CCT Pro 240 TTA Leu	His TCA Ser CTA CTA CTA CTG TCTG TTCG TTCG TCTG CTA CTA	Ser GCC Ala ATT Ile ACC Thr 210 CCT Pro GAC GAC GAC GLU	TCC Ser TTT Phe 195 CAG Gln CCC Pro	CAAAGIN 180 ATT Ile GCT Ala GGG Gly 260 CTG Leu	Gln 165 GTA Val TTT Phe GGA Gly TTC Phe 245 TTC Phe	GCT Ala GTG Val	Ser GGG Gly TTT Phe CAG Gln 215 TTA Leu A CCA Pro	Thr ACC Thr AAT ASN 200 TGG Trp CGC Phe	Product AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GIU 170 GAC GAC GAT C TTC C AAT A ASI C TGC C Cys A GCT A AC 250 A AC 250 A 250 A AC 250 A AC 250 A 250 A AC 250 A 25	I Ile ATG Met AGA AGA ATG CTT Leu CCCG Pro 235 AAT AASn TTG Leu	CAC His CAG Gln GGC Gly 220 AGC Ser TTT Phe ATC Ile	578 626 674 722 770 818

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	GGG																914
136	Gly	Ile	Thr	Gly	Val		His	His	Ala	Arg		Ile	Pḥe	Asn	Phe	Cys	
	285					290					295					300	
	TTG																962
140	Leu	Phe	Glu	Met	Glu	Ser	His	Ser	Val	\mathtt{Thr}	Gln	Ala	Gly	Val		\mathtt{Trp}	
141					305					310					315		
143	CCA	AAT	CTC	GGC	TCA	CTG	CAA	CCT	CTG	CCT	CCC	GGG	CTC	AAG	CGA	TTC	1010
144	Pro	Asn	Leu	Gly	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	
145				320					325					330			
147	TCC	TGT	CTC	AGC	CTC	CCA	AGC	AGC	TGG	GAT	TAC	GGG	CAC	CTG	CCA	CCA	1058
148	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	
149	•		335					340					345				
151	CAC	CCC	GCT	AAT	TTT	TGT	ATT	TTC	ATT	AGA	GGC	GGG	GTT	TCA	CCA	TAT	1106
152	His	Pro	Ala	Asn	Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr	•
153		350					355					360					
155	TTG	TCA	GGC	TGG	TCT	CAA	ACT	CCT	GAC	CTC	AGG	TGAG	CCCA	CCT (GCCT	CAGCCT	1159
156	Leu	Ser	Gly	Trp	Ser	Gln	Thr	Pro	Asp	Leu	Arg						
157	365		_	_		370			_		375						
159	TCC	AAAG!	IGC :	rggg <i>i</i>	ATTA	CA GO	GCGT	GAGC	CAC	CTCA	CCCA	GCC	GCT	AAT :	TTAG	ATAAAA	1219
161	AAA	ratg:	rag (CAAT	GGGG	GG TO	CTTG	CTAT	TTC	GCCC	AGGC	TGG	CTC	AAA (CTTC:	TGGCTT	1279
																GTTACA	1339
165	TCT	TAT	TTT A	AGTA:	PACTA	AG AZ	AAGT	AATA	CAA	ГААА	CATG	TCA	AACC!	rgc A	AAAT	TCAGTA	1399
167	GTA?	ACAG	AGT :	CTT:	TAT	AA C	TTTT	AAAC	A AA	GCTT	ľAGA	GCA					1442
170	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO: 2	2:	,							
172																	
173	173 (A) LENGTH: 375 amino acids																
175	, ,																
176			•	•			line										
178		(ii) MOI	LECUI	LE T	YPE:	prot	tein									
180		•					_	ON: S	SEQ :	ID NO): 2	:					
182	Met	•											Asn	Gly	Ala	Ile	
183	1				5				_	10		_		_	15		
185	Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	Asp	Ser	Pro	Ala	
186				20			_		25	_	•		_	30			
188	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Glý	Met	Cys	Thr	His	Ala	Arg	
189			35				_	40					45				
191	Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	Leu	His	Val	Gly	
192		50		-			55					60				-	
194	Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	Ser	Val	Ser	Ala	
195	65		-			70				_	75					80	
	Ser	Gln	Ser	Ala	Arq	Tyr	Arq	Thr	Gly	His	His	Ala	Arq	Leu	Cys	Leu	
198					85	-	_		-	90			_		95		
200	Ala	Asn	Phe	Cys	Gly	Arq	Asn	Arq	Val	Ser	Leu	Met	Cys	Pro	Ser	Trp	
201				100	1	5		5	105				- 2 -	110		-	
	Ser	Pro	Glu		Lvs	Gln	Ser	Thr		Leu	Ser	Leu	Pro		Cvs	Trp	
204			115		_, _			120	-10				125	-1-	- 1 -	F	
	Asp	Tvr		Arσ	Ala	Ala	Val		G] v	Leu	Phe	IJe		Phe	Phe	Leu	
207		130	9				135		1		• •	140					
	3		Δra	Cvs	Pro	Thr		Thr	G] n	Asp	G] u		G] n	Tro	Cvs	Asp	
209	Aro																

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	145					150					155					160	
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213					165					170					175		
215	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr		Asp	Met	His	His	Tyr	Thr	Trp	
216				180					185					190			
218	Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	Ser	Leu	Asn	Ser	
219			195					200					205				
221	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	Ser	Leu	Gln	Pro	
222		210					215					220					
224	Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	Leu	Leu	Ser	Ser	
225	225					230			•	`	235					240	
227	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu	
228					245					250					255		
230	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly	
231			*	260					265	_				270			
233	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly	
234		-	275					280					285			_	
	Val	Ser	His	His	Ala	Arq	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met	
237		290				5	295					300					
	Glu		His	Ser	Val	Thr		Ala	Glv	Val	Gln	Trp	Pro	Asn	Leu	Gly	
	305					310			1		315	_				320	
		Leu	Gln	Pro	Leu		Pro	Glv	Leu	Lvs		Phe	Ser	Cvs	Leu		
243	001	Lou	01		325			011		330	5			-1-	335		
	T.e.n	Pro	Ser	Ser		Δsn	Ͳτ	Glv	His		Pro	Pro	His	Pro	Ala	Asn	
246	шси	110	DCI	340	111	шьр	-1-	011	345	Lou	110	110		350			
	Dho	Cvc	Tla		Tla	A ro	G1 17	Glv		Ser	Pro	ጥላንዮ	T.e.u		Gly	Ψгο	
249	THE	Cys	355	1110	110	ni 9	OLY	360	vai	DCI	110	+1-	365	501	011		
	Cor	Gln		Pro	λen	T.a.ı	λνα	300					303				
252	261	370	1111	FIO	тэр	пец	375										
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256	` '							ISTIC									
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260		, , , , ,	•) TO													
		(ii							- DO	TD 11/	.						
267		•		-							0: 3		73.CM	7.77	N MCC	7C C 3 3 III	60
																CGCAAT	60
																CTCCCC	120
																TAGTA	180
																ATGATC	240
277	TCC	CGTC!	rcg (CCT	3CCC2	AA AC	TGC.	rgag <i>i</i>	A TTA	ACAG	CAT	GAG	JCAC(CAT (JCCC(GCCTC	300
																STCTCC	360
																CAGCC	420
																CAGGAT	480
																CAATCC	540
																STAATT	600
																GAGTGC	660
291	AGT	GGCG	CAA :	CTTC	GGCT	CA C	rg _/ CA <i>l</i>	ACCT	C TG	CCTC	CCGG	GTT	CAAG!	rta '	TTCT(CCTGCC	720

RAW SEQUENCE LISTING DATE: 10/16/2001 PATENT APPLICATION: US/09/964,667 TIME: 15:24:03

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\1964667.raw

	CCAGCCTCCT GAGTAGCTGG					780
295	TTTTAGTAGA GATGGGGTTT	CACCATGTTC	GCCAGGTTGA	TCTTGATCTC	TTGACCTTGT	840
297	GATCTGCCTG CCTCGGCCTA	CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	CCACGCCGGC	900
299	CTATTTTTAA TTTTTGTTTG	TTTGAAATGG	AATCTCACTC	TGTTACCCAG	GTCGGAGTGC	960
301	AATGGCAAAT CTCGGCTACT	CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	CTCCTGTCTC	1020
303	AGCCTCCCAA GCAGCTGGGA	TTACGGGACC	TGCACCACAC	CCCGCTAATT	TTTGTATTTT	1080
305	CATTAGAGGC GGGTTTACCA	TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	CCTCAGGTGA	1140
307	CCCACCTGCC TCAGCCTTCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	TCACCCAGCC	1200
309	GGCTAATTTG GAATAAAAAA	TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	CAGGCTGGTC	1260
311	TCAAACTTCT GGCTTCAGTC	AATCCTTCCA	AATGAGCCAC	AACACCCAGC	CAGTCACATT	1320
313	TTTTAAACAG TTACATCTTT	ATTTTAGTAT	ACTAGAAAGT	AATACAATAA	ACATGTCAAA	1380
315	С					1381
317	(2) INFORMATION FOR SE	O ID NO: 4:	•			
319	(i) SEQUENCE CHAR			•		
320	(A) LENGTH:					
321	(B) TYPE: nu	-				
322	(C) STRANDED					
323	(D) TOPOLOGY					
325	(ii) MOLECULE TYPE					
330	(xi) SEQUENCE DESC		O TO NO. 4	•		
	TTTTTTTTT GAGATGGAGT				а тесесеса а т	60
	CTCAGCTCAC CGCAACCTCC					120
	AGTAGGCTGG GATTACAGGC					180
	AGAGATGGAG TTTCTCCATG					240
	CCCGTCTCGG CCTCCCAAAG					300
						360
	GGCTAATTTT TGTGGTAGAA					420
	CAAGCAGTCC ACCTGCCTCA					480
	TGGCCTTTTT ATTTTATTTT					
	GCAGTGGTGT GATCACAGCT					540
	TCAGCCTCCC AAAGTAGCTG					600
	TTTTATTTTT AATTTTTTGA					660
	GCGCAATCTT GGCTCACTGC					720
	CCTCCTGAGT AGCTGGGACT					780
	AGTAGAGATG GGGTTTCACC					840
	CTGCCTGCCT CGGCCTCCCA					900
	TATTTTTAAT TTTTGTTTGT					960
	ATGGCCAAAT CTCGGCTCAC					1020
	CAGCCTCCCA AGCAGCTGGG					1080
369	TTCATTAGAG GCGGGGTTTC	ACCATATTTG	TCAGGCTGGT	CTCAAACTCC	TGACCTCAGG	1140
371	TGACCCACCT GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCCAGC	1200
373	CGGCTAATTT AGATAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
375	GTCTCAAACT TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
377	ATTTTTAAAC AGTTACATCT	TTATTTTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
379	AACCTGCAAA TTCGAGTAGT	ACAGAGTCTT	TTATAACT			1418
381	(2) INFORMATION FOR SE	Q ID NO: 5:	:			
383	(i) SEQUENCE CHAR	ACTERISTICS	5:			
384	(A) LENGTH:	22 base pai	irs			
385	(B) TYPE: nu	cleic acid				
386	(C) STRANDED	NESS: singl	.e			

· VERIFICATION SUMMARY

DATE: 10/16/2001

PATENT APPLICATION: US/09/964,667

TIME: 15:24:04

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964667.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]